In the Claims:

Please amend the claims as shown:

Claims

1. (Currently Amended) Oligonucleotide for genotyping and pathotyping the species *Pseudomonas aeruginosa* with a nucleic acid sequence, selected from the group consisting of (all sequences in 5' → 3' direction):

i)

GAAGCCCAGCAATTGCGTGTTTC **(SEQ ID NO: 72)**

GAAGCCCAGCAACTGCGTGTTTC **(SEQ ID NO: 73)**

GGTGCTGCAGGGTGTTTCGCCGG **(SEQ ID NO: 76)**

GGTGCTGCAGGGCGTTTCGCCGG **(SEQ ID NO: 77)**

CAAGATCGCCGCAGCGGTCAAC **(SEQ ID NO: 78)**

CAAGATCGCCGCTGCGGTCAAC **(SEQ ID NO: 79)**

TGCTGCTGGCGGCGGTGTGCTAT **(SEQ ID NO: 80)**

TGCTGCTGGCAGCGGTGTGCTAT **(SEQ ID NO: 81)**

CCTCGCCCTGTTCCCACCGCTCTGG **(SEQ ID NO: 84)**

CTCGCCCTGTTCCCGCCGCTCTGG **(SEQ ID NO: 85)**

TCGAGCAACTGGCAGAGAAATCCG **(SEQ ID NO: 86)**

CGAGCAACTGGCGGAGAAATCCG **(SEQ ID NO: 87)**

GCGGAAAACTTCCTGCACATGATGTT **(SEQ ID NO: 88)**

GCGGAAAACTTCCTCCACATGATGTT **(SEQ ID NO: 89)**

AGCTCAGCAGACTGCTGACGAGG **(SEQ ID NO: 90)**

AGCTCAGCAGACCGCTGACGAG **(SEQ ID NO: 91)**

AAGAGGACGGCCGCCGGGTGACGCC **(SEQ ID NO: 5)**

AAGAGGACGGCCGCCAGGTGACGCCG **(SEQ ID NO: 6)**

GACAAGATGCGCCTCGACGACC **(SEQ ID NO: 7)**

GACAAGATGCGTCTCGACGACCG **(SEQ ID NO: 8)**

AGCCGACCTACGCGCCGGGCAG **(SEQ ID NO: 9)**

CAGCCGACCTATGCGCCGGGCAG **(SEQ ID NO: 10)**

CCGTTCGAACGGCTCATGGAGCA **(SEQ ID NO: 11)**

GCCGTTCGAACGACTCATGGAGCA **(SEQ ID NO: 12)**

TGGAGCAGCAAGTGTTCCCGGC **(SEQ ID NO: 13)**

TGGAGCAGCAACTGTTCCCGGC **(SEQ ID NO: 14)**

GAACAAGACCGGTTCCACCAACGG **(SEQ ID NO: 15)**

AACAAGACCGGCTCCACCAACGG **(SEQ ID NO: 16)**

GCGACCTGGGCCTGGTGATCCT **(SEQ ID NO: 17)**

GCGACCTGGGACTGGTGATCC **(SEQ ID NO: 18)**T

GCCGACCAACTGAACTCCAACTCG **(SEQ ID NO: 19)**

GTCGCTGAACGGCACCTACTTCA **(SEQ ID NO: 20)**

CAGCCTGCGGTCATGTCCTCGG **(SEQ ID NO: 21)**

CGCCAGTTTGAGAACGGAGTCACC **(SEQ ID NO: 22)**

GCGCGATCTTCTCCACTTCATCGG **(SEQ ID NO: 23)**

GCCTCCGCGATTGAACATCGTGAT **(SEQ ID NO: 24)**

GTAGCCGGAGTCGAGCGGAATCAT **(SEQ ID NO: 25)**

GTGAGCATGGAATCGGCAGTCGTT **(SEQ ID NO: 26)**

CGAGGAGTTTCGGACCCGCTTTGA **(SEQ ID NO: 27)**

AATAGGACCGGCAGAACGGGCATT **(SEQ ID NO: 28)**

GCGCCTTCTCCTCTTTGCAGATGT **(SEQ ID NO: 29)**

CAGTATGGTACGGACACGAAGCGC **(SEQ ID NO: 30)**

GCATCATTGCGCGTCACATCTGGT **(SEQ ID NO: 31)**

TCTGAACTGCGGCTATCACCTGGA **(SEQ ID NO: 32)**

AATTGATGGCTTCTCAGGCGCAGG **(SEQ ID NO: 33)**

AGTCATGGGACTGAATACGGCGACT **(SEQ ID NO: 34)**

TTCTCGGTGTCGAGGGATTCTCGG **(SEQ ID NO: 35)**

TGGTAGCTCTCGACGTACTGGCTG **(SEQ ID NO: 36)**

CCCGTTGCTCATAACCCGTTCCTG **(SEQ ID NO: 37)**

AGGGCATTCTCAGGTGGACTCAGG **(SEQ ID NO: 38)**

ACCTGTGTCGCTGGAGGGTATGTT **(SEQ ID NO: 39)**

AGCGTCCCTGACCAACCTCATCAG **(SEQ ID NO: 40)**

CGCCAACAATTCGCCATTACAGCG **(SEQ ID NO: 41)**

TCCAACAGGCAGGAGTACAGGGTG **(SEQ ID NO: 42)**

CGCTGCACATACAGGTCCGTTCTC **(SEQ ID NO: 43)**

AGCCCAGCAATTGCGTGTTTCTCCG **(SEQ ID NO: 44)**

AGCCCAGCAACTGCGTGTTTCTCC **(SEQ ID NO: 45)**

GCTGCTGGCGGCGGTGTGC **(SEQ ID NO: 46)**

TGCTGCTGGCAGCGGTGTGCT **(SEQ ID NO: 47)**

CAGAAAGCTCAGCAGACTGCTGACGAG **(SEQ ID NO: 48)**

GAAAGCTCAGCAGACCGCTGACGAG **(SEQ ID NO: 49)**

ACGGCCGCCGGGTGACGCC **(SEQ ID NO: 50)**

ACGGCCGCCAGGTGACGCCG **(SEQ ID NO: 51)**

GCCGACCTACGCGCCGGGC **(SEQ ID NO: 52)**

AGCCGACCTATGCGCCGGGCA **(SEQ ID NO: 53)**

GTTCGAACGGCTCATGGAGCAGCA **(SEQ ID NO: 54)**

GTTCGAACGACTCATGGAGCAGCAAG **(SEQ ID NO: 55)**

CAGCCCAGTCAGGACGCGCA **(SEQ ID NO: 56)**

AGTGACGTGCGTTTCAGCAGTCCC **(SEQ ID NO: 57)**

GTGTCACGGCCCATGTCTAGCAGC **(SEQ ID NO: 58)**

CGAAGTCTGAGGTGTGGACCCGC **(SEQ ID NO: 59)**

CGCTGGAGGGTATGTTCCGCAAGG **(SEQ ID NO: 60)**

CGTACTCAGCTTCTCCACCCAGCG **(SEQ ID NO: 61)**

CCTGGACCTCTCCAAGGTTCGCCT **(SEQ ID NO: 62)**

GCCATTCCGACGACCAAACAAGGC **(SEQ ID NO: 63)**

GTGCTGCAGGGTGTTTCGCCG **(SEQ ID NO: 110)**

GCTGCAGGGCGTTTCGCCG **(SEQ ID NO: 111)**

CAAGATCGCCGCAGCGGTCAACGAC **(SEQ ID NO: 135)**

CAAGATCGCCGCTGCGGTCAACGAC **(SEQ ID NO: 136)**

GCTCAGCAGACTGCTGACGAGGCTAACG **(SEQ ID NO: 112)**

GCTCAGCAGACCGCTGACGAGGCTAAC **(SEQ ID NO: 113)**

CGACCTACGCGCCGGGCAG **(SEQ ID NO: 114)**

CGACCTATGCGCCGGGCAGC **(SEQ ID NO: 115)**

CGTTCGAACGGCTCATGGAGCAG **(SEQ ID NO: 116)**

CGTTCGAACGACTCATGGAGCAGC **(SEQ ID NO: 117)**

CGACCTGGGCCTGGTGATCCT **(SEQ ID NO: 118)**

GCGACCTGGGACTGGTGATCCTGG **(SEQ ID NO: 119)**

CAGTTGTCGCCAGGTCTGGAGAATCC **(SEQ ID NO: 137)**

CACATCAATGTCAGCCCACGCCA **(SEQ ID NO: 138)**

CTGGAGCCTGCGAAAGTGGCTC **(SEQ ID NO: 139)**

ACGAGGGTGATGGCTGGGAATACG **(SEQ ID NO: 140)**

GCCAATTGGGTCAGCAAGCAACG **(SEQ ID NO: 141)**

CGTGTCGCGAACTCGCATGGC **(SEQ ID NO: 142)**

AGGCCATGGGCTAGCCGGATGC **(SEQ ID NO: 159)**

CGAAGCGTAGGGTCTTCGTAGCC **(SEQ ID NO: 160)**

TGCGAGGACCAGAAACCTTGATGG **(SEQ ID NO: 161)**

CGGTATGAAGATGGGTGGTTGGGTCG **(SEQ ID NO: 162)**

CCTGAATCCGACCATTCGCGAGTC **(SEQ ID NO: 143)**

TCGGACTGTACTCCTACGAAGCAGC **(SEQ ID NO: 144)**

CCAATCCCTATCGCTGGAACCGTACC **(SEQ ID NO: 145)**

GCTCGGGACTCGCATTTCGTCC **(SEQ ID NO: 146)**

GCGTTATTGCTCGGTCTCTCCTCG **(SEQ ID NO: 147)**

TGCATAGGAGTCATGCCGACAGCA **(SEQ ID NO: 163)**

GCCTGCCTACTTGTTCCCAACGC **(SEQ ID NO: 164)**

GGCTGTATTGCCCGCCATTCTCC **(SEQ ID NO: 165)**

CGACAGACAGAAAGGGTTCTTGCGC **(SEQ ID NO: 166)**

CACCATGCAAATGCTCGATGGACTGC **(SEQ ID NO: 167)**

GCAGGCGTCCAAGTTGGAGCTCTCC **(SEQ ID NO: 168)**

GGAACACAACGTGGGGCGTGAC **(SEQ ID NO: 169)**

CCAGTTGGCACCACCATGCTTGC **(SEQ ID NO: 170)**

GACCGCAAGCAGAAACGGCATGC **(SEQ ID NO: 148)**

CCATGGTCGGAACAGGCACGATATGC **(SEQ ID NO: 149)**

CCACTCGATCATGTTGAGCATCGGCTCC **(SEQ ID NO: 150)**

GGTTAGTCCCTTCTGCCCGCATCG **(SEQ ID NO: 151)**

ii) oligonucleotides matching one of the oligonucleotides under i) in at least 60%, preferably in at least 80%, and particularly preferably in at least 90%, 92%, 94 %, 96% of the bases and allowing specific hybridization with nucleic acid sequences of bacterial strains of the species *Pseudomonas aeruginosa*,

iii) oligonucleotides differing from one of the oligonucleotides under i) and ii) in that they are extended by at least one nucleotide, and

iv) oligonucleotides hybridizing with a sequence, which is complementary to an oligonucleotide under i), ii) and iii), under stringent conditions.

2. (Original) Microarray device comprising a support element, on which oligonucleotide probes are immobilized on predetermined regions, for specifically detecting bacterial strains of the species *Pseudomonas aeruginosa*.

3. (Original) Device according to claim 2,
characterized in that the device is a reaction tube having a shape and / or size typical for a laboratory reaction tube and having a support element, on which oligonucleotide probes are immobilized on predetermined regions, arranged on one of its base areas for specifically detecting bacterial strains of the species *Pseudomonas aeruginosa*.

4. (Previously Presented) Device according to claim 2,
characterized in that the oligonucleotide probes are selected in such a way that they detect 30% to 70% of the population of *Pseudomonas aeruginosa* strains in each case.

5. (Previously Presented) Device according to claim 2, characterized in that the oligonucleotide probes are specific for nucleic acids having a base substitution compared to the sequence of the reference strain of *Pseudomonas aeruginosa*.

6. (Previously Presented) Device according to claim 2, characterized in that the oligonucleotide probes are specific for nucleic acids present in only one or few strains of the species *Pseudomonas aeruginosa*.

7. (Previously Presented) Device according to claim 2, characterized in that the oligonucleotide probes are specific for nucleic acids present in pathogenicity islets in the genome of *Pseudomonas aeruginosa*.

8. (Previously Presented) Device according to claim 2, characterized in that the oligonucleotide probes are specific for nucleic acids present in disease-associated genes like *exoS* and *exoU*.

9. (Previously Presented) Device according to claim 2, characterized in that the oligonucleotide probes are specific for nucleic acids contained in genes coding for flagella of *Pseudomonas aeruginosa*.

10. (Previously Presented) Device according to claim 2, characterized in that the oligonucleotide probes are selected from the oligonucleotides according to claim 1.

11. (Previously Presented) Method for specifically detecting bacterial strains of the species *Pseudomonas aeruginosa* in a sample, comprising the following steps:
a) contacting the sample with a nucleic acid chip in a microarray device according to claim 2; and
b) detecting the interaction between the oligonucleotide probes and the target nucleic acids contained in the sample.

12. (Original) Method according to claim 11, characterized in that the target nucleic acids contained in the sample are amplified before the detection.

13. (Original) Method according to claim 12, characterized in that the amplification is performed by means of multiplex PCR.

14. (Original) Method according to claim 13, characterized in that primers, which have similar melting points and / or similar binding kinetics, are used for the amplification.

15. (Previously Presented) Method according to claim 12, characterized in that the amplification is performed linearly.

16. (Currently Amended) Method according to claim 12, characterized in that the primers are selected with a nucleic acid sequence selected from the group consisting of (all sequences in 5' → 3' direction):
ACGCGGATGTCCTGGATTTGG **(SEQ ID NO: 176)**
CTGAAGAAGGGGCGCTACGCG **(SEQ ID NO: 177)**
GCGTACCGGGCAAGGTGATAG **(SEQ ID NO: 178)**
CTCGGTGAAACATCGGGAGGG **(SEQ ID NO: 179)**

TCATCCAGCAAGCCATTGCGC **(SEQ ID NO: 180)**

GGAGTCGCTTTCCGCCATCG **(SEQ ID NO: 181)**

TGGAGTCGCTTTCCGCCATCG **(SEQ ID NO: 182)**

AAGGGCGTTTCACGCTGACGC **(SEQ ID NO: 183)**

ATCCGGAAGGGCGTTTCACG **(SEQ ID NO: 184)**

TCCACACCTCAGACTTCGGCG **(SEQ ID NO: 185)**

TATTGACGACCTACCGCGCGC **(SEQ ID NO: 186)**

GCAACTGATGTTCGCCCAGC **(SEQ ID NO: 187)**

CGCAACTGATGTTCGCCCAGC **(SEQ ID NO: 188)**

ACACGCAACTGATGTTCGCCC **(SEQ ID NO: 189)**

TGTCCCGGCTCAGTTCAACG **(SEQ ID NO: 190)**

AACACCTTGGCGTTTGTCCC **(SEQ ID NO: 191)**

GCAACACCTTGGCGTTTGTCC **(SEQ ID NO: 192)**

TCAAGCTCGTTGTGGACCGC **(SEQ ID NO: 193)**

GTTACGACGGCGTGCTGTCGG **(SEQ ID NO: 194)**

ACGCAACGTATTCGGCGACCC **(SEQ ID NO: 195)**

CGCAACGTATTCGGCGACCC **(SEQ ID NO: 196)**

AGCTGATGGTATCGCCGTCGC **(SEQ ID NO: 197)**

CTAGTGATCGCACCGGAGCC **(SEQ ID NO: 198)**

AGCCTCGACACCGGTTCTCG **(SEQ ID NO: 199)**

TCGTTCATCCCCAGGCTTCG **(SEQ ID NO: 200)**

ACCATCTCGTTCATCCCCAGG **(SEQ ID NO: 201)**

TTCTGAGCCCAGGACTGCTCG **(SEQ ID NO: 202)**

TCGACGCGACGGTTCTGAGCC **(SEQ ID NO: 203)**

TGACGTTCTCGCCGGTAGCG **(SEQ ID NO: 204)**

CAGTAGCGGTACCGGTCTGCG **(SEQ ID NO: 205)**

CAGTAGCGGTACCGGTCTGC **(SEQ ID NO: 206)**

TTCCTCGCCGGCATAGTAGGC **(SEQ ID NO: 207)**

CGAGGACGAGGCATCTTCCGG **(SEQ ID NO: 209)**

GCAGGTAGCAGGTTTCCAGG **(SEQ ID NO: 210)**

AACTGTTCCTTCTGCGCGGCG **(SEQ ID NO: 211)**

TGATCGGCTTGGTCTCGCAGG **(SEQ ID NO: 212)**

GCTGATCGGCTTGGTCTCGC **(SEQ ID NO: 213)**

GAGGCGTTCTGCTCGTGGTCG **(SEQ ID NO: 214)**

TTTTTCCAGCATGCGCAGGG **(SEQ ID NO: 215)**

GCTGGCTTTTTCCAGCATGCG **(SEQ ID NO: 216)**

TTGCGGCTGGCTTTTTCCAGC **(SEQ ID NO: 217)**

TTGGGATAGTTGCGGTTGGC **(SEQ ID NO: 218)**

CGTAGGCGATCTTCACCCGC **(SEQ ID NO: 219)**

TGGCGTAGGCGATCTTCACCC **(SEQ ID NO: 220)**

GGCGAGATAGCCGAACAGGC **(SEQ ID NO: 221)**

GCGGCGAGATAGCCGAACAGG **(SEQ ID NO: 222)**

CACTTGCTGCTCCATGAGCC **(SEQ ID NO: 223)**

GAGGTCGAGCAGGCTGATGC **(SEQ ID NO: 224)**

TAGGTCGCGAGGTCGAGCAGG **(SEQ ID NO: 225)**

GTCCTTCTGCACCGAGTCGG **(SEQ ID NO: 226)**

CGCATCTTGTCCTGGGTCAGG **(SEQ ID NO: 227)**

TCGTCGAGGCGCATCTTGTCC **(SEQ ID NO: 228)**

ACGTCGAGGTGGGTCTGTTCG **(SEQ ID NO: 229)**

GTAGCCTTCGGCATCCAGCG **(SEQ ID NO: 230)**

TCGGCATTGGGATAGTTGCGG **(SEQ ID NO: 231)**

CCTCCTGTCTCATGCCGATGC **(SEQ ID NO: 232)**

GCATTCGCCACGGAAGGAAGG **(SEQ ID NO: 233)**

GAAGGCATCATGGCATTCGCC **(SEQ ID NO: 234)**

GTCATGGGGTTTCCCAGAGACC **(SEQ ID NO: 235)**

GATCGCGATGTCGACGGTGCC **(SEQ ID NO: 236)**

CGATCGCGATGTCGACGGTGC **(SEQ ID NO: 237)**

TGCCGATCGCGATGTCGACG **(SEQ ID NO: 238)**

GACGAATACCCAGCTGCGTGG **(SEQ ID NO: 239)**

GCAGACGAATACCCAGCTGCG **(SEQ ID NO: 240)**

CGCGACGTCGTGACGTCAGC **(SEQ ID NO: 241)**

ACTTTCGGCTCTTCGGGCTGG **(SEQ ID NO: 242)**

AGGTAGAGACTCGGGGGAACC **(SEQ ID NO: 243)**

TCGTTTTCGGTCATGGCCAGG **(SEQ ID NO: 244)**

TTCCGCGACGAACATCCGTGG **(SEQ ID NO: 245)**

CGCTTCCGCGACGAACATCCG **(SEQ ID NO: 246)**

GGATCGCTTCCGATAGGGCAGC **(SEQ ID NO: 247)**

AGAGGCATGGGTCTGTACCG **(SEQ ID NO: 248)**

TCTGTCAATCCCCTTTGGGG **(SEQ ID NO: 249)**

AGCCCCTTTCTGTCAATCCCC **(SEQ ID NO: 250)**

GGCTTCCTACCGAAGGTCAGG **(SEQ ID NO: 251)**

TGAGGGCTTCCTACCGAAGG **(SEQ ID NO: 252)**

TTCAAGGTCATGGGCAATGCC **(SEQ ID NO: 253)**

AGTCCCTTCAAGGTCATGGGC **(SEQ ID NO: 254)**

GCCGACTGAGCTGTAGCTCGG **(SEQ ID NO: 255)**

GGCCGACTGAGCTGTAGCTCG **(SEQ ID NO: 256)**

ACCAGACTGGTCAATGGTGG **(SEQ ID NO: 257)**

CCCGTGTTTCCGTAGACCTTGC **(SEQ ID NO: 258)**

AGCAGTTACCCACAGCATGG **(SEQ ID NO: 259)**

CAGCAGTTACCCACAGCATGG **(SEQ ID NO: 260)**

CTACACTCCAACCGCTGGTCC **(SEQ ID NO: 261)**

GACCTACACTCCAACCGCTGG **(SEQ ID NO: 262)**

TTCCCTTGCTGCCGAGAAGC **(SEQ ID NO: 263)**

TAATAGGCGAGCCTGCCGTCC **(SEQ ID NO: 264)**

TCCACGCCGAGGGACGTGCC **(SEQ ID NO: 265)**

GCTCCACGCCGAGGGACGTGCC **(SEQ ID NO: 266)**

CGCGGTGCTGGTTGCGCTGC **(SEQ ID NO: 267)**

CCAATGCCCAGGGCCAGCGGA **(SEQ ID NO: 268)**

CGCTGGCAGTTCCGCTGGCC **(SEQ ID NO: 269)**

CAGGGTCGCCAGCTCGCTCGCC **(SEQ ID NO: 270)**

AGGGTCGCCAGCTCGCTCGC **(SEQ ID NO: 271)**

AGTGATCTGCCGCGGCCCTGCC **(SEQ ID NO: 272)**

GTGATCTGCCGCGGCCCTGC **(SEQ ID NO: 273)**

GTTCCACAGGCGCTGCGGCGC **(SEQ ID NO: 274)**

GTTCCACAGGCGCTGCGGCG **(SEQ ID NO: 275)**

CAAAGCCCCTGGTCGCGCGG **(SEQ ID NO: 276)**

GCAGCTTTTCCACCGCCGGCGG **(SEQ ID NO: 277)**

AAACTGCCCCGCCCCCCATCC **(SEQ ID NO: 278)**

GGAAAAACTGCCCCGCCCCCC **(SEQ ID NO: 279)**

ACGCTCGCAGCGCCTCACGCG **(SEQ ID NO: 280)**

GGCCTGGCTGCGAACGCTCGC **(SEQ ID NO: 281)**

GGGGTCGAGACGTGTACATGG **(SEQ ID NO: 208)**

TTCCTGGGCCAGAGTTGGACC **(SEQ ID NO: 282)**

AGCTTAAGGCCGTGGCACTCG **(SEQ ID NO: 283)**

CCGGAGAATTCGCGTCCACC **(SEQ ID NO: 284)**

TGCTGACGATGAAGCCCCAGC **(SEQ ID NO: 285)**

AGGAGGCCGATGACAACACCC **(SEQ ID NO: 286)**

TGCCGATTCCATGCTCACGCC **(SEQ ID NO: 287)**

ACGACGTCACCGTCGAGACCG **(SEQ ID NO: 288)**

ACCGCCTTTCTGGTGAGCTGG **(SEQ ID NO: 289)**

AGCCAAGACGGTTGTTCGCGG **(SEQ ID NO: 290)**

TCAATGACGCCGAGTTGGCGC **(SEQ ID NO: 291)**

CTCGGACAGGTTCACGCTGG **(SEQ ID NO: 292)**

GCCATTCGCTGCAACACCTCC **(SEQ ID NO: 293)**

GCGCGCGTTCGAGAAACAGG **(SEQ ID NO: 294)**

CGGAGGTTGAAAAGCTGGCCC **(SEQ ID NO: 295)**

ATGCCATCGTTGAAGGCACCGC **(SEQ ID NO: 296)**

TGCCATCGTTGAAGGCACCG **(SEQ ID NO: 297)**

TCTGGCGGAATCAGGTAGGCC **(SEQ ID NO: 298)**

CTTCCGGGGAGAAACCACCG **(SEQ ID NO: 299)**

ACCTCCAGCACCGACACACC **(SEQ ID NO: 300)**

ATCCGATCCACCTCCAGCACC **(SEQ ID NO: 301)**

CGTTCAGGTCGTAGACCGCGC **(SEQ ID NO: 302)**

GCGATACCAACTGTCCTGCGGC **(SEQ ID NO: 303)**

TGCCGAAGGTGAATGGCTTGCC **(SEQ ID NO: 304)**

CCTGATGGTCCGATCCCAGC **(SEQ ID NO: 305)**

GCCGAGGGTCAAGAACCACTGG **(SEQ ID NO: 306)**

TCTTGGCCCAGTCATAGCGGC **(SEQ ID NO: 307)**

TAACCCCAAGGCCCATTGGAGG **(SEQ ID NO: 308)**

GCCACCGCCTTCGAATAACCCC **(SEQ ID NO: 309)**

AATTGCTCGAGGGATGCGGC **(SEQ ID NO: 310)**

GGTCGAAACGGATGCGCAGG **(SEQ ID NO: 311)**

GCCCCGCGTCATTTTCACGTCG **(SEQ ID NO: 312)**

AATGCTCTGGGCAACGAGCC **(SEQ ID NO: 313)**

CTACCCAGCTTGGGCGTAGC **(SEQ ID NO: 314)**

AAGCGATAGCCGTGCTCCTGC **(SEQ ID NO: 315)**

CCGGCTATATCCGCGGCTACC **(SEQ ID NO: 316)**

ATTGGCGCTGCTGTTTACGCCC **(SEQ ID NO: 317)**

GGTGGCGTCGGGTTTTTCTGC **(SEQ ID NO: 318)**

AGGTCGTAGCGGAAGGTGGTGG **(SEQ ID NO: 319)**

ATCTGAACCGAGGGGATCCGC **(SEQ ID NO: 320)**

CCCGGGAGTCATTGGTCTGG **(SEQ ID NO: 321)**

GCCTGTTGGACCCCTTTGACC **(SEQ ID NO: 322)**

TACTCCTGCCTGTTGGACCCC **(SEQ ID NO: 323)**

CGCTCAAGCGCTATCCCACC **(SEQ ID NO: 324)**

CGCCATCGGCCTGTACAACG **(SEQ ID NO: 325)**

CGGTAGAGAGCTGGGTTGGC **(SEQ ID NO: 326)**

AACCTGGAGCTAGGGCAGAGC **(SEQ ID NO: 327)**

GGTGCTCGACCCAAGCATCG **(SEQ ID NO: 328)**

TCCTTGAGTTCCTTGGCGCGG **(SEQ ID NO: 329)**

CAACACGCGACTGGCGATCC **(SEQ ID NO: 330)**

TACATCATCCGCAACGGCGGC **(SEQ ID NO: 331)**

TATTGACGACCTACCGCGCGCC **(SEQ ID NO: 332)**

CACCAAGAACCCGCTGCTCG **(SEQ ID NO: 333)**

ATCGTGGCAGGATGTCCACCG **(SEQ ID NO: 334)**

TAGGCGGGCCTTTTGAAGGTGC **(SEQ ID NO: 335)**

17. (Original) Use of the oligonucleotides according to claim 1 for specifically detecting bacterial strains of the species *Pseudomonas aeruginosa*.

18. (Previously Presented) A method for genotyping and pathotyping *Pseudomonas aeruginosa*, comprising the following steps:

a) contacting the sample with a nucleic acid chip in a microarray device according to claim 2; and

b) detecting the interaction between the oligonucleotide probes and the target nucleic acids contained in the sample.

19. (Previously Presented) A method for amplifying nucleic acids of bacterial strains of the species *Pseudomonas aeruginosa,* comprising the following steps:

a) contacting the sample with a nucleic acid chip in a microarray device according to claim 2; and

b) detecting the interaction between the oligonucleotide probes and the target nucleic acids contained in the sample.